1

SEQUENCE LISTING

<110> Reinhard, Christoph

<120> HUMAN CYCLIN-DEPENDANT KINASE (hPNQALRE)

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<140> US 09/464,065
<141> 1999-12-15

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<212> DNA
<213> Homo sapien

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gcctcaggcc agctcaagat agcggacttt ggcctggctc gagtcttttc cccagacggc     480
agccgcctct acacacacca ggtggccacc aggtctgtgg gctgcatcat gggggagctg     540
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<211> 325
<212> PRT
<213> Homo sapien

<400> 2
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1               5                   10                  15
Ile Val Phe Lys Ala Lys His Val Glu Thr Gly Glu Ile Val Ala Leu
            20                  25                  30
Lys Lys Val Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala
        35                  40                  45
Leu Arg Glu Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val
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        50                  55                  60
Val Gln Leu Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala
65                  70                  75                  80
Phe Glu Phe Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln
                    85                  90                  95
Arg Pro Leu Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu
            100                 105                 110
Lys Gly Val Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu
        115                 120                 125
Lys Pro Ala Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala
    130                 135                 140
Asp Phe Gly Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr
145                 150                 155                 160
Thr His Gln Val Ala Thr Arg Ser Val Gly Cys Ile Met Gly Glu Leu
                165                 170                 175
Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn Asp Ile Glu Gln Leu
            180                 185                 190
Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn Pro Gln Val Trp Pro
        195                 200                 205
Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile Ser Leu Lys Glu Gln
    210                 215                 220
Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp Val Ser Pro Gln Ala
225                 230                 235                 240
Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro Pro His Gln Arg Ile
            245                 250                 255
Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe Phe Thr Ala Pro Leu
        260                 265                 270
Pro Ala His Pro Ser Glu Leu Pro Ile Pro Gln Arg Leu Gly Gly Pro
        275                 280                 285
Ala Pro Lys Ala His Pro Gly Pro Pro His Ile His Asp Phe His Val
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Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro Glu Leu Ile Arg Pro
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Phe Ile Leu Glu Arg
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<211> 1053
<212> DNA
<213> Homo sapien

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gaagacggct ccctaaccca ggccctgcgg gagattaagg ctctgcagga gatggaggac     180
aatcagtatg tggtacaact gaaggctgtg ttcccacacg tggaggcttt gtgctggcc      240
tttgagttca tgctgtcgga tctggccgag gtggtgcgcc atgcccagag gccgctagcc     300
caggcacagg tcaagagcta cctgcagatg ctgctcaagg tgtcgccttc tgccatgcc      360
aacaacattg tacatcggga cctgaaacct gccaacctgc tcatcagcgc ctcaggccag     420
ctcaagatag cggactttgg cctggctcga gtcttttccc cagacggcag ccgcctctac     480
acacaccagg tggccaccag gtggtaccga gcccccgagc tcctgtatgg tgcccgccag     540
tatgaccagg gcgtcgatct gtggtctgtg ggctgcatca tggggagct gttgaatggg      600
tccccccttt tcccgggcaa gaacgatatt gaacagcttt gctatgtgct cgcatcttg     660
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aaggctctcc tccatcagta cttcttcaca gctcccctgc ctgcccatcc atctgagctg    900
ccgattcctc agcgtctagg gggacctgcc cccaaggccc atccagggcc cccccacatc    960
catgacttcc acgtggaccg gcctcttgag gagtcgctgt tgaacccaga gctgattcgg   1020
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<210> 4
<211> 346
<212> PRT
<213> Homo sapien

<400> 4

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  1               5                  10                  15
Ile Val Phe Lys Ala Lys His Val Glu Thr Gly Glu Ile Val Ala Leu
             20                  25                  30
Lys Lys Val Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala
             35                  40                  45
Leu Arg Glu Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val
          50                  55                  60
Val Gln Leu Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala
 65                  70                  75                  80
Phe Glu Phe Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln
                85                  90                  95
Arg Pro Leu Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu
             100                 105                 110
Lys Gly Val Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu
             115                 120                 125
Lys Pro Ala Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala
             130                 135                 140
Asp Phe Gly Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr
145                 150                 155                 160
Thr His Gln Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Tyr
                165                 170                 175
Gly Ala Arg Gln Tyr Asp Gln Gly Val Asp Leu Trp Ser Val Gly Cys
             180                 185                 190
Ile Met Gly Glu Leu Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn
             195                 200                 205
Asp Ile Glu Gln Leu Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn
             210                 215                 220
Pro Gln Val Trp Pro Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile
225                 230                 235                 240
Ser Phe Lys Glu Gln Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp
                245                 250                 255
Val Ser Pro Gln Ala Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro
             260                 265                 270
Pro His Gln Arg Ile Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe
             275                 280                 285
Phe Thr Ala Pro Leu Pro Ala His Pro Ser Glu Leu Pro Ile Pro Gln
          290                 295                 300
Arg Leu Gly Gly Pro Ala Pro Lys Ala His Pro Gly Pro Pro His Ile
305                 310                 315                 320
His Asp Phe His Val Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro
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                     325                  330                    335
Glu Leu Ile Arg Pro Phe Ile Leu Glu Arg
                     340                  345


<210> 5
<211> 1092
<212> DNA
<213> Homo sapien

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gagatagttg ccctcaagaa ggtggcccta aggcggttgg aagacggctt ccctaaccag     180
gccctgcggg agattaaggc tctgcaggag atggaggaca atcagtatgt ggtacaactg     240
aaggctgtgt tcccacacgg tggaggcttt gtgctggcct ttgagttcat gctgtcggat     300
ctggccgagg tggtgcgcca tgcccagagg ccactagccc aggcacaggt caagagctac     360
ctgcagatgc tgctcaaggg tgtcgccttc tgccatgcca acaacattgt acatcgggac     420
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<210> 6
<211> 359
<212> PRT
<213> Homo sapien

<400> 6
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Ile Val Phe Lys Ala Lys His Val Glu Pro Arg Val Gly Trp Gln Cys
                20                  25                  30
Leu Pro Ser Ile Leu Gln Thr Gly Glu Ile Val Ala Leu Lys Lys Val
            35                  40                  45
Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala Leu Arg Glu
        50                  55                  60
Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val Val Gln Leu
65                  70                  75                  80
Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala Phe Glu Phe
                85                  90                  95
Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln Arg Pro Leu
            100                 105                 110
Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu Lys Gly Val
            115                 120                 125
Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu Lys Pro Ala
        130                 135                 140
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Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala Asp Phe Gly
145                 150                 155                 160
Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr Thr His Gln
                165                 170                 175
Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Tyr Gly Ala Arg
                180                 185                 190
Gln Tyr Asp Gln Gly Val Asp Leu Trp Ser Val Gly Cys Ile Met Gly
            195                 200                 205
Glu Leu Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn Asp Ile Glu
        210                 215                 220
Gln Leu Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn Pro Gln Val
225                 230                 235                 240
Trp Pro Glu Leu Thr Glu Leu Pro Asp Tyr Asn Lys Ile Ser Phe Lys
                245                 250                 255
Glu Gln Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp Val Ser Pro
                260                 265                 270
Gln Ala Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro Pro His Gln
            275                 280                 285
Arg Ile Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe Phe Thr Ala
        290                 295                 300
Pro Leu Pro Ala His Pro Ser Glu Leu Pro Val Pro Gln Arg Leu Gly
305                 310                 315                 320
Gly Pro Ala Pro Lys Ala His Pro Gly Pro Pro His Ile His Asp Phe
                325                 330                 335
His Val Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro Glu Leu Ile
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Arg Pro Phe Ile Leu Glu Gly
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<210> 7
<211> 1038
<212> DNA
<213> Homo sapien

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gagatagttg ccctcaagaa ggtggcccta aggcggttgg aggacggctt ccctaaccag       180
gccctgcggg agattaaggc tctgcaggag atggaggaca atcagtatgt ggtacaactg       240
aaggctgtgt ccccacacgg tggaggcttt gtgctggcct ttgagttcat gctgtcggat       300
ctggccgagg tggtgcgcca tgcccagagg ccactagccc aggcacaggt caagagctac       360
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<211> 345
<212> PRT
<213> Homo sapien

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Ile Val Phe Lys Ala Lys His Val Glu Pro Arg Val Gly Trp Gln Cys
            20                  25                  30
Leu Pro Ser Ile Leu Gln Thr Gly Glu Ile Val Ala Leu Lys Lys Val
            35                  40                  45
Ala Leu Arg Arg Leu Glu Asp Gly Phe Pro Asn Gln Ala Leu Arg Glu
        50                  55                  60
Ile Lys Ala Leu Gln Glu Met Glu Asp Asn Gln Tyr Val Val Gln Leu
65                  70                  75                  80
Lys Ala Val Phe Pro His Gly Gly Gly Phe Val Leu Ala Phe Glu Phe
                85                  90                  95
Met Leu Ser Asp Leu Ala Glu Val Val Arg His Ala Gln Arg Pro Leu
            100                 105                 110
Ala Gln Ala Gln Val Lys Ser Tyr Leu Gln Met Leu Leu Lys Gly Val
            115                 120                 125
Ala Phe Cys His Ala Asn Asn Ile Val His Arg Asp Leu Lys Pro Ala
        130                 135                 140
Asn Leu Leu Ile Ser Ala Ser Gly Gln Leu Lys Ile Ala Asp Phe Gly
145                 150                 155                 160
Leu Ala Arg Val Phe Ser Pro Asp Gly Ser Arg Leu Tyr Thr His Gln
                165                 170                 175
Val Ala Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Tyr Gly Ala Arg
            180                 185                 190
Gln Tyr Asp Gln Gly Val Asp Leu Trp Ser Val Gly Cys Ile Met Gly
            195                 200                 205
Glu Leu Leu Asn Gly Ser Pro Leu Phe Pro Gly Lys Asn Asp Ile Glu
        210                 215                 220
Gln Leu Cys Tyr Val Leu Arg Ile Leu Gly Thr Pro Asn Pro Gln Val
225                 230                 235                 240
Trp Pro Glu Gln Val Pro Met Pro Leu Glu Glu Val Leu Pro Asp Val
                245                 250                 255
Ser Pro Gln Ala Leu Asp Leu Leu Gly Gln Phe Leu Leu Tyr Pro Pro
            260                 265                 270
His Gln Arg Ile Ala Ala Ser Lys Ala Leu Leu His Gln Tyr Phe Phe
            275                 280                 285
Thr Ala Pro Leu Pro Ala His Pro Ser Glu Leu Pro Ile Pro Gln Arg
            290                 295                 300
Leu Gly Gly Pro Ala Pro Lys Ala His Pro Gly Pro Pro His Ile His
305                 310                 315                 320
Asp Phe His Val Asp Arg Pro Leu Glu Glu Ser Leu Leu Asn Pro Glu
                325                 330                 335
Leu Ile Arg Pro Phe Ile Leu Glu Gly
            340                 345

<210> 9
<211> 7
<212> PRT
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<213> Unknown

<220>
<223> Sequence which characterizes the cyclin binding
      domain of cyclin-dependant kinases.

<400> 9
Pro Asn Gln Ala Leu Arg Glu
 1               5

<210> 10
<211> 7
<212> PRT
<213> Unknown

<220>
<223> Sequence which characterizes the cyclin binding
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<400> 10
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 1               5

<210> 11
<211> 7
<212> PRT
<213> Unknown

<220>
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<400> 11
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 1               5

<210> 12
<211> 7
<212> PRT
<213> Unknown

<220>
<223> Sequence which characterizes the cyclin binding
      domain of cyclin-dependant kinases.

<400> 12
Pro Ile Thr Ala Leu Arg Glu
 1               5

<210> 13
<211> 7
<212> PRT
<213> Unknown
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<220>
<223> Sequence which characterizes the cyclin binding
      domain of cyclin-dependant kinases.

<400> 13
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 1   5

<210> 14
<211> 7
<212> PRT
<213> Unknown

<220>
<223> Sequence which characterizes the cyclin binding
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<400> 14
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 1   5

<210> 15
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<212> PRT
<213> Unknown

<220>
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      domain of cyclin-dependant kinases.

<400> 15
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 1   5

<210> 16
<211> 7
<212> PRT
<213> Unknown

<220>
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      domain of cyclin-dependant kinases.

<400> 16
Asn Arg Thr Ala Leu Arg Glu
 1   5

<210> 17
<211> 21
<212> PRT
<213> Homo spaien

<400> 17
His Asp Phe His Val Asp Arg Pro Leu Glu Glu Ser Leu Ile Asn Pro

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  1                    5                10                  15
Glu Leu Ile Arg Pro
              20
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